

Attorney Docket No.: P-633 (TI-0020)
Inventors: Taylor and Yu
Serial No.: 09/873,645
Filing Date: June 4, 2001
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This listing of the claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-12 (canceled).

Claim 13 (currently amended): A system for computer implemented adjustment of signal data and time data of a plurality of chromatographic elution profiles ~~to generate values useful for grouping the plurality of chromatographic elution profiles~~, said system comprising:

a computer having a processor and memory, wherein the processor comprises instructions for:

(a) ~~plots~~ plotting sets of data from a plurality of chromatographic elutions on a coordinate system comprising a first axis associated with time values and a second axis associated with detector response values, thereby generating a plurality of chromatographic elution profiles, wherein each set of data is obtained from the separation of a DNA mixture by Denaturing Matched Ion Polynucleotide Chromatography, wherein each DNA mixture comprises homoduplex and heteroduplex molecules obtained from hybridization of a sample DNA and its corresponding wild type DNA,

(b) ~~selects~~ selecting first and second time points defining a time span wherein peaks due to said homoduplex and heteroduplex molecules are located within said time span,

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(c) for each profile and within said time span, ~~adjusts~~ adjusting the baseline by applying a slope factor to each detector response value, said slope factor derived from a line connecting the detector response values at said first and second time points such that all of the profiles have a common baseline,

(d) then after creating the common baseline for each profile and within said time span, ~~normalizes~~ normalizing the heights of the peaks to a pre-selected scale based on the height of the highest peak, and finally

(e) ~~shifts~~ shifting each of the profiles along said first axis such that all of the profiles intersect at a pre-selected point on the last eluting peak of each profile within said time span so that values from the plurality of chromatographic elution profiles can be used to group the plurality of chromatographic elution profiles ~~for comparison with values from control profiles to detect mutations in the sample DNA.~~

Claim 14 (original): The system of claim 13 wherein said pre-selected value is zero, wherein said pre-selected scale is from 0 to 1, wherein said pre-selected point comprises a point on the last eluting edge of said last eluting peak, and wherein in step (c) the second axis value at the first time point and the second axis value at the second time point are set to zero.

Claim 15 (currently amended): The system of claim 13 wherein said processor further comprises instructions for performing the steps of:

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(a) within said span, divides the first axis into a series of adjacent and evenly spaced time regions, wherein boundary lines perpendicular to said first axis are located between adjacent time regions,

(b) divides each boundary line number 1 through I

(c) for each boundary line, numbered 1 through I

i) determines the number of profiles intersecting each of said segments,

ii) determines the segment having the highest number of intersecting profiles and determines the nearest segment having zero intersecting profiles,

iii) for each boundary line, assigns a numerical grouping factor of n^i to the profiles that have a second axis value greater than said segment having zero intersecting profiles and assigns a grouping factor of 1 to the remaining intersecting profiles, wherein n is an integer greater than 1,

(d) for each profile obtains a total value comprising the sum of all the grouping factors assigned to said each profile,

(e) groups together those profiles having the same total value.

Claim 16 (previously presented): The system of claim 15 wherein $n=2$.

Claims 17-27 (canceled).